

File Name: SY-12

Created: 14:29 01-01-22  
Data: Original

Measuring Mode: Abs.  
Scan Speed: Fast  
Slit Width: 1.0  
Sampling Interval: 0.2

FIG.1

Result = (Area \* Factor) / Divisor      Factor = 0.000

Region	Start	End	Divisor	Area	Result
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## CAMAG TLC Evaluation Software

ANBRO PHARMACEUTICALS LTD 6714 KIRTI NAGAR INDUSTRIAL AREA NEW DELHI  
PHONE: 91-67226515-0437, FAX: 91-11-6453784, E-mail: anbro@vsnl.com

LC/UV/IC-Integration (CAT3.18 S/N:32274001 / SCANNER II V3.14 S/N:990602)

## ESTIMATION OF L-LYSINE BY HPTLC

Calib.Table      Calibration table, created : 3/6/2000 PHARMA LED  
 Scan            File name : AMINO            3/JUN/ 0 14:49:45  
 Integration    User name while measuring : AMB20 PHARMA LED  
 File name : AMINO            3/JUN/ 0 14:54:52  
 User while integrating : AMB20 PHARMA LED  
 File name : AMINO            3/JUN/ 0 15:19:25

## Track 1. Analysis a:

Peak	start		max	end	area
	min	h			[%]
1	61.1	0.4	72.6	64.1	100.00
			Total height =	64.1	Total area = 3136.2

## Track 2. Standard level 1

Peak	start		max	end	area
	min	h			[%]
1	62.9	2.8	71.0	63.5	100.00
			Total height =	63.5	Total area = 3133.9

FIG.2(a)

U 013488-3

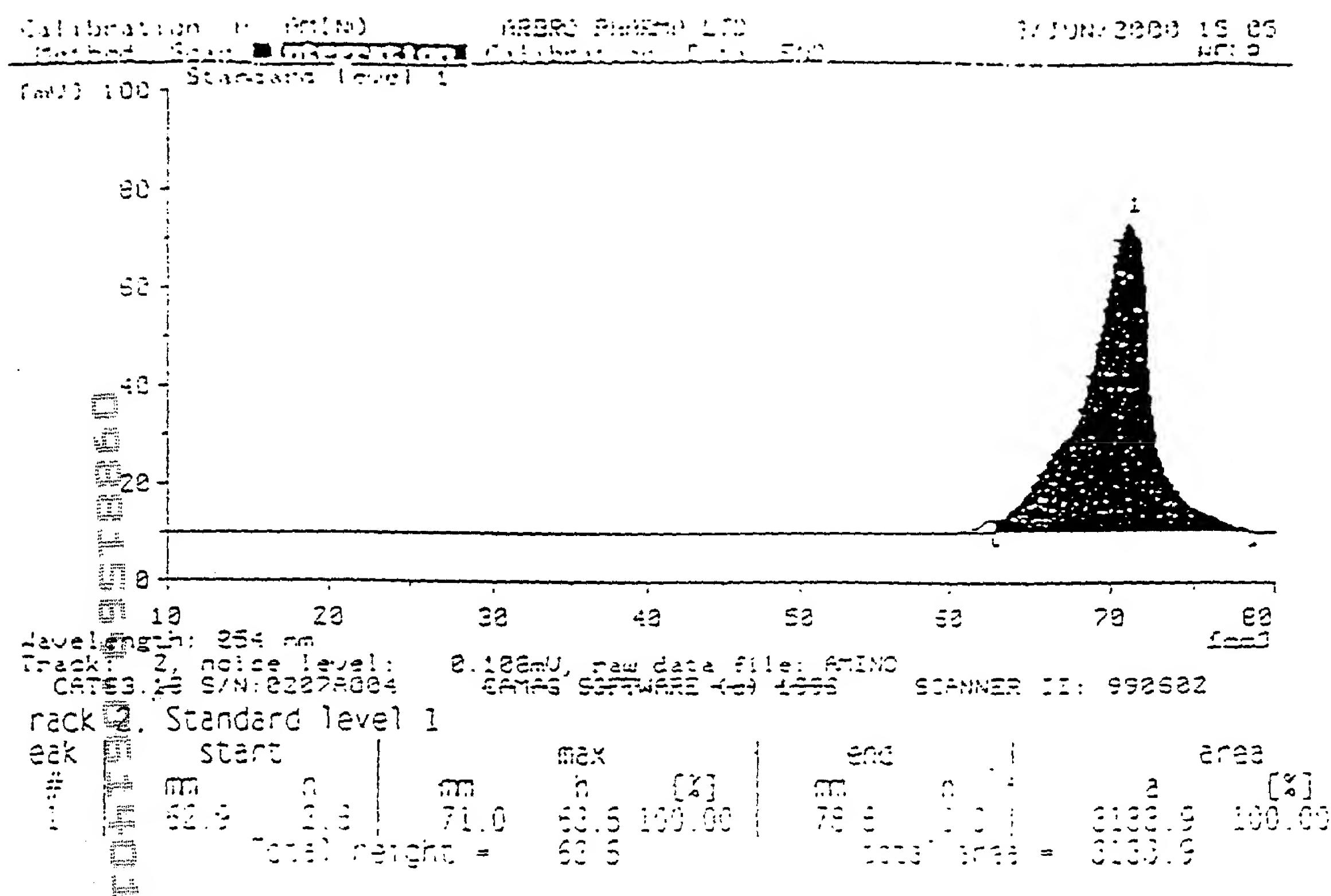


FIG. 2(b)

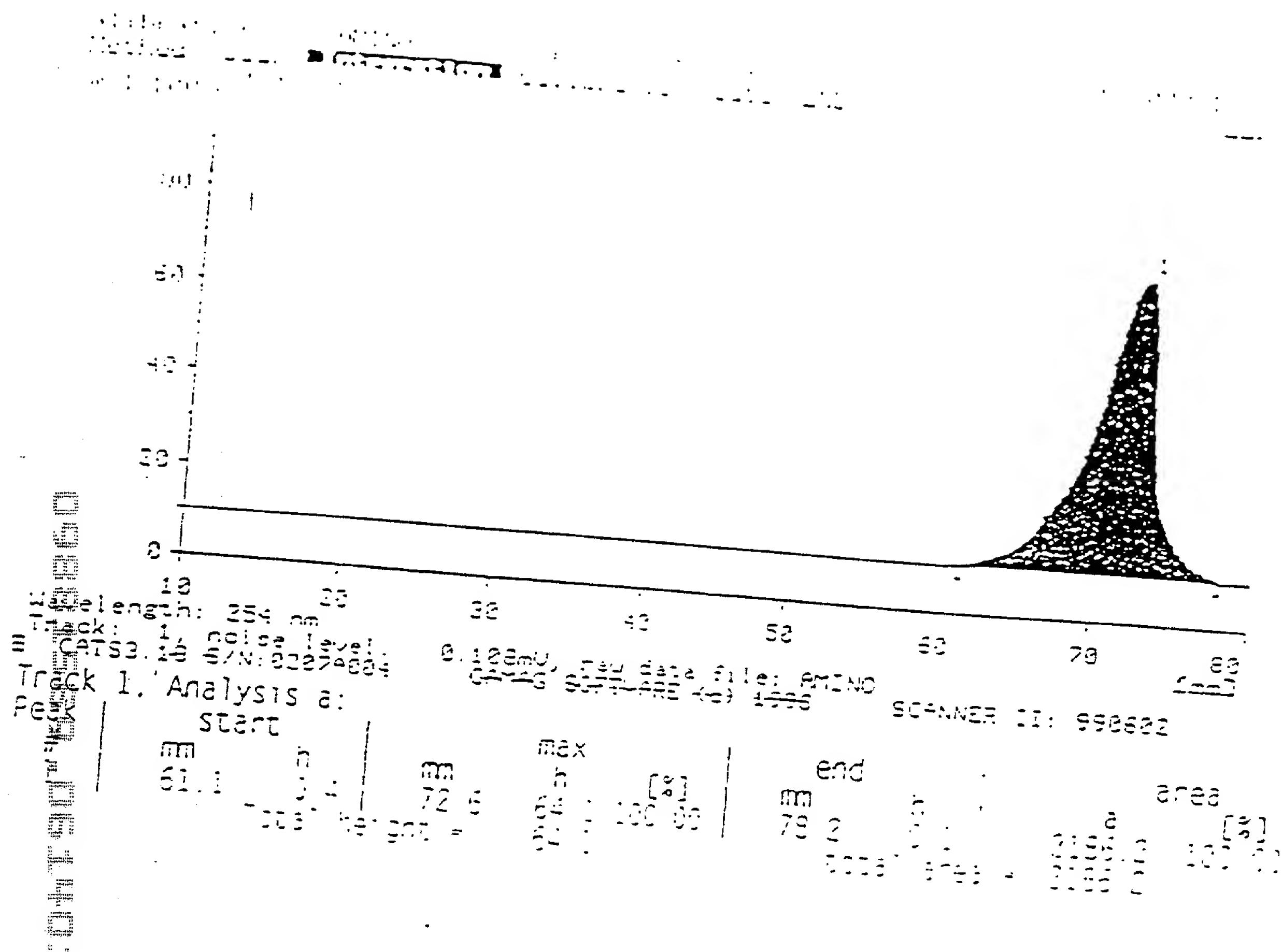


FIG. 2(c)

U 013488-3

A chromatogram plot with the y-axis labeled 'Intensity' ranging from 0 to 100. A single, very sharp peak is visible at a retention time of approximately 10 minutes. The x-axis is labeled 'Retention Time (min)'.

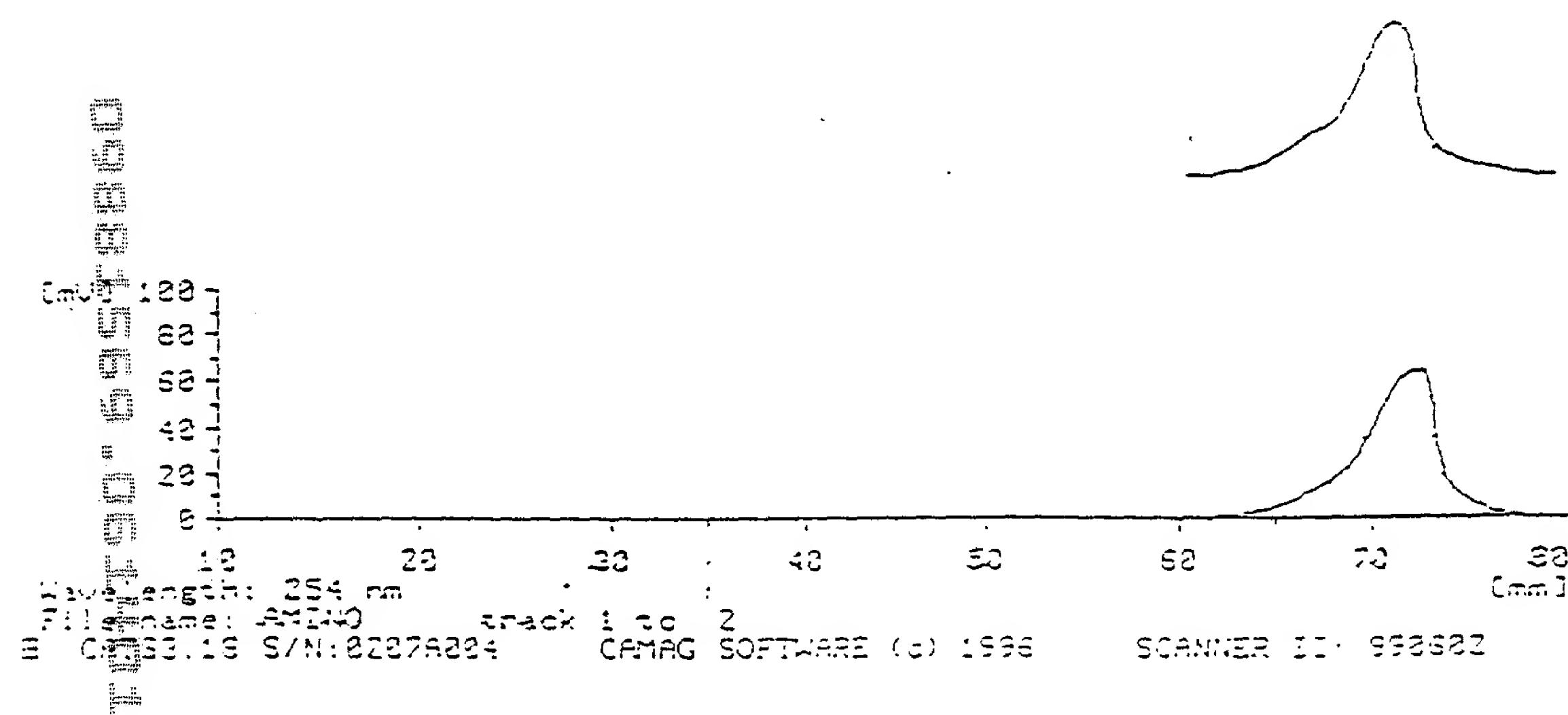


FIG.2(d)

SUBMITTER : PUSHPA KHANNA

SAMPLE NAME : GOURDIN

DATE : \_\_\_\_\_

SEQUENCE : GLY • ILE → GLU → GLU → THR → THR → GLY → GLN → THR → HIS  
 CYCLE # : 1 2 3 4 5 6 7 8 9 ARG GLN GLN LEU

			ARG				GLY		
		TYR	HIS	HIS		ARG	ASP	ARG	ARG
	LYS	ILE	ALA	GLU ASN	MET	ASN	THR	HIS	
SEQUENCE :	ARG	LEU	LYS	TYR-ASP	ILE	LEU	ASP	ALA	
CYCLE #:	10	11	12	13	14	15	16	17	18

. SER PRO  
 . GLU SER GLU THR ARG HIS  
 . LEU ARG PRO ILE LEU PHE SER ALA ARG  
 SEQUENCE : LYS - GLU - ALA - ASP - ILE - TYR - ASN - HIS - GLY  
 CYCLE #: 19 20 21 22 23 24 25 26 27

	GLY		VAL		PRO			
	VAL		LEU ASN	ILE	ALA			
SEQUENCE :	ALA	GLY	ARG	ILE	SER	THR	VAL	ASN
CYCLE #:	28	29	30	31	32	33	34	35

YIELD (pmol) : ILE(2) 98.11 YIELD(pmole) : GLU(3) 56.13

CARRYOVER : JLE(6) 22.6% REP YIELD: JLE(2.23) 92.3%

SEQSTD YIELD : NI (6) 2.30 SEQSTD CARRYOVER : NI (6) 23.0%

SEOSTD REP YIELD NI (6.11) 97.0%

COMMENTS : Mixtures with interchangeable amino acids at positions 12, 13, 15-19, 25-27 and 31-34. Appears to be a mixture of sequences

### GOURDIN PLANT

45.0  
4.0

qto0-2637 32 (0.661) Sm (Mn, 2x3.00); Cm (3:97)

100 1154.02 1177.95 1180.87 1183.87

1158.51 1173.01

1205.73 1213.94

1203.93

1246.34

1237.40 1265.83 1271.04

1232.88 1249.72 1294.88 1297.89 1301.00

1240.89 1263.98 1267.05 1271.00

%

TOF MS ES+

345

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TOF MS ES+

384

qto0-2637 32 (0.661) Cm (3:97) 1183.87

1154.02 1157.99 1180.78 1185.98

1158.51 1174.10 1205.40 1214.02

1186.55 1206.06 1214.35 1237.07 1239.85

1186.67 1204.75 1218.55 1240.89 1263.98

1214.35

1237.07

1239.85

1267.05

1271.00

1301.04

%

0 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 m/z

FIG. 4 (a)

## GOURDIN PLANT

**4.0**

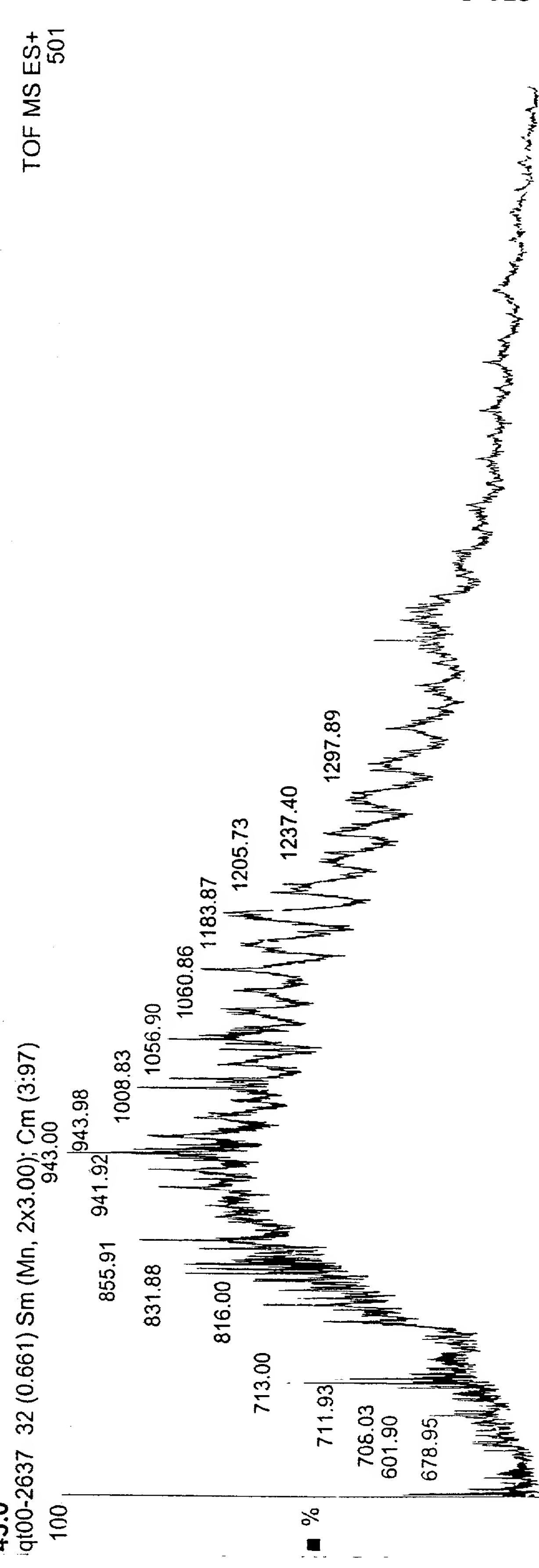
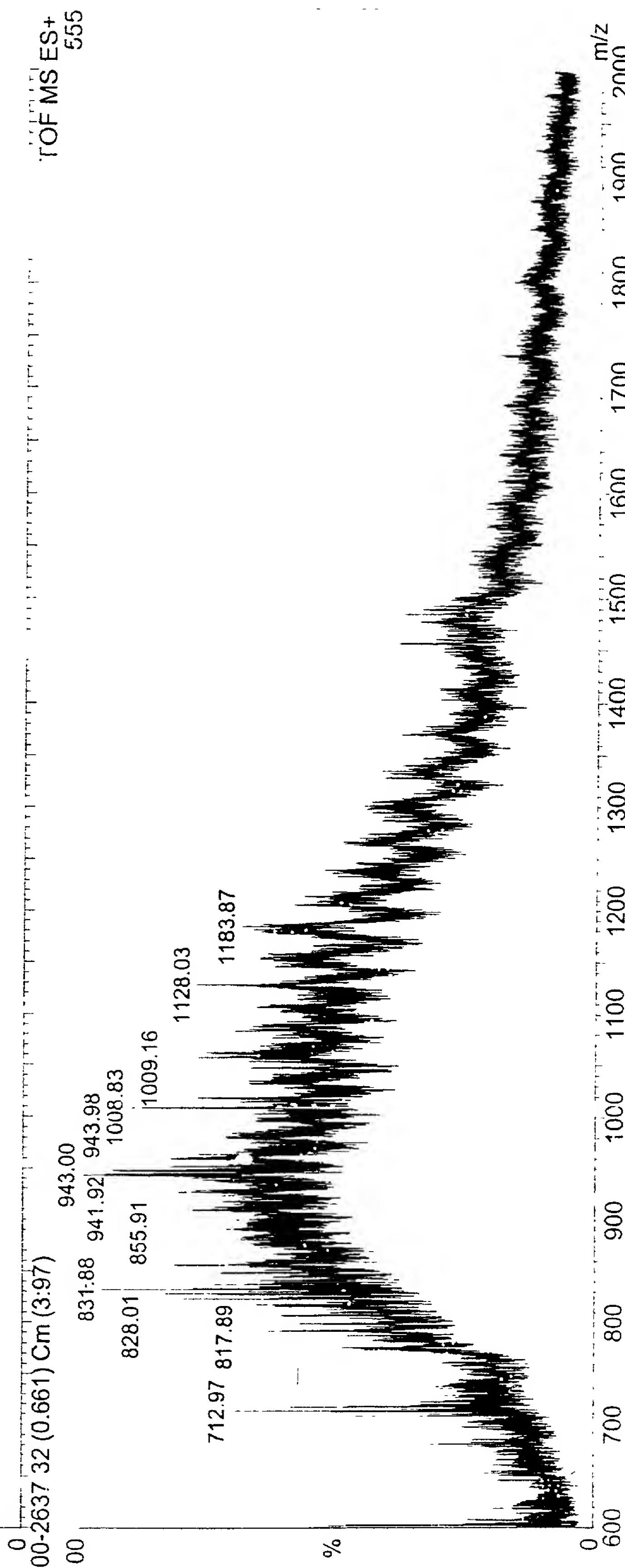


FIG. 4(b)



GOURDIN PLANT

45.0  
Q700-2637 32 (0.661) Mk [Ev-52491,lt17] (Gs,0.750,900;1999,1.00,L33,R33); Sb (6,20.00); Cm (3:96)  
100  
943.03

4.0

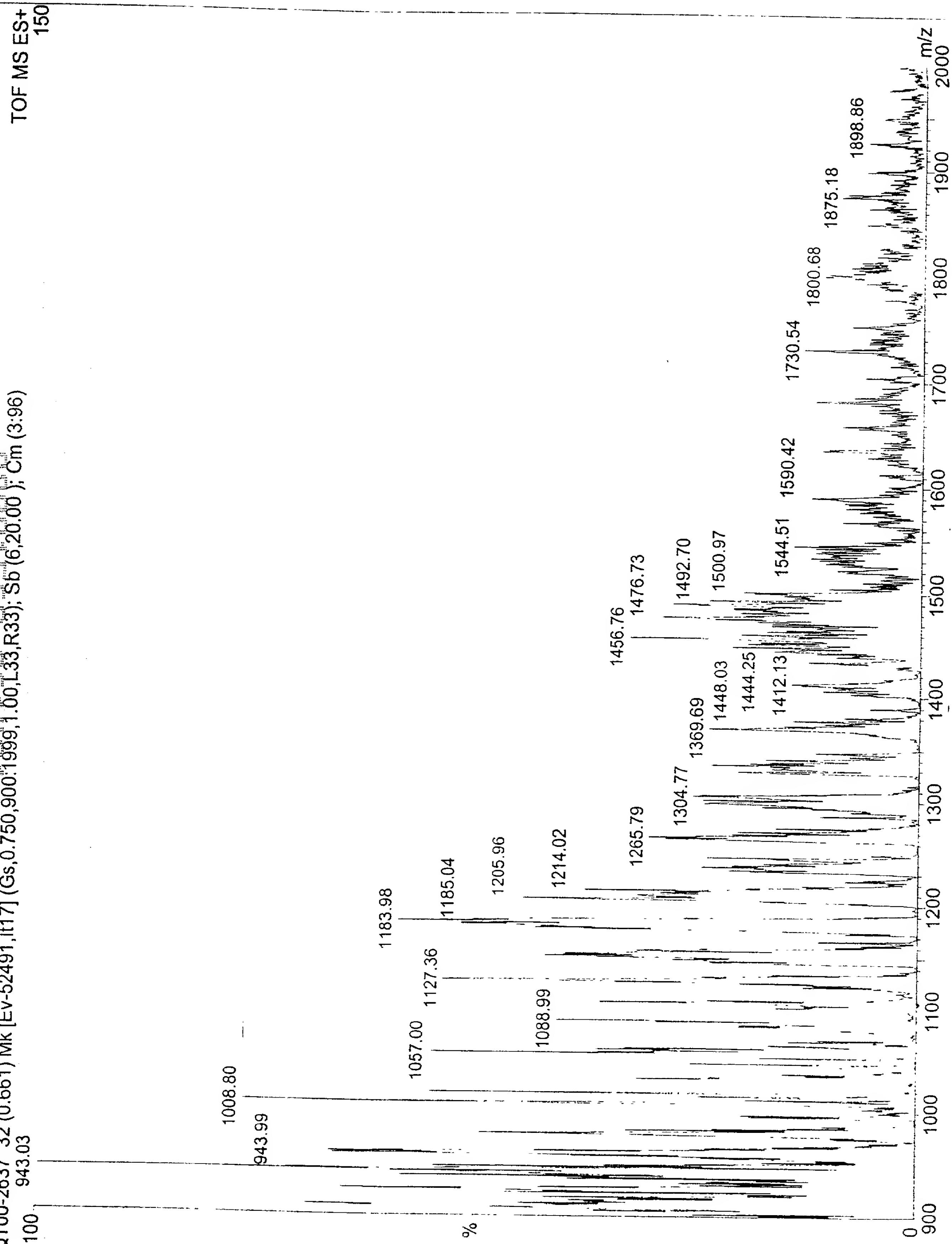
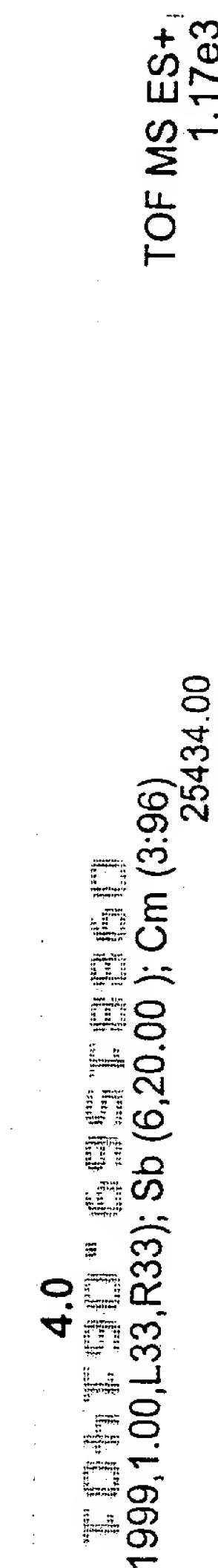


FIG. 4(c)

GOURDIN PLANT

45.0  
QT00-2637 32 (0.661) M1 [Ev-52491,It17] (Gs,0.750,900;1999,1.00,L33,R33); Sb (6,20.00); Cm (3.96)  
100



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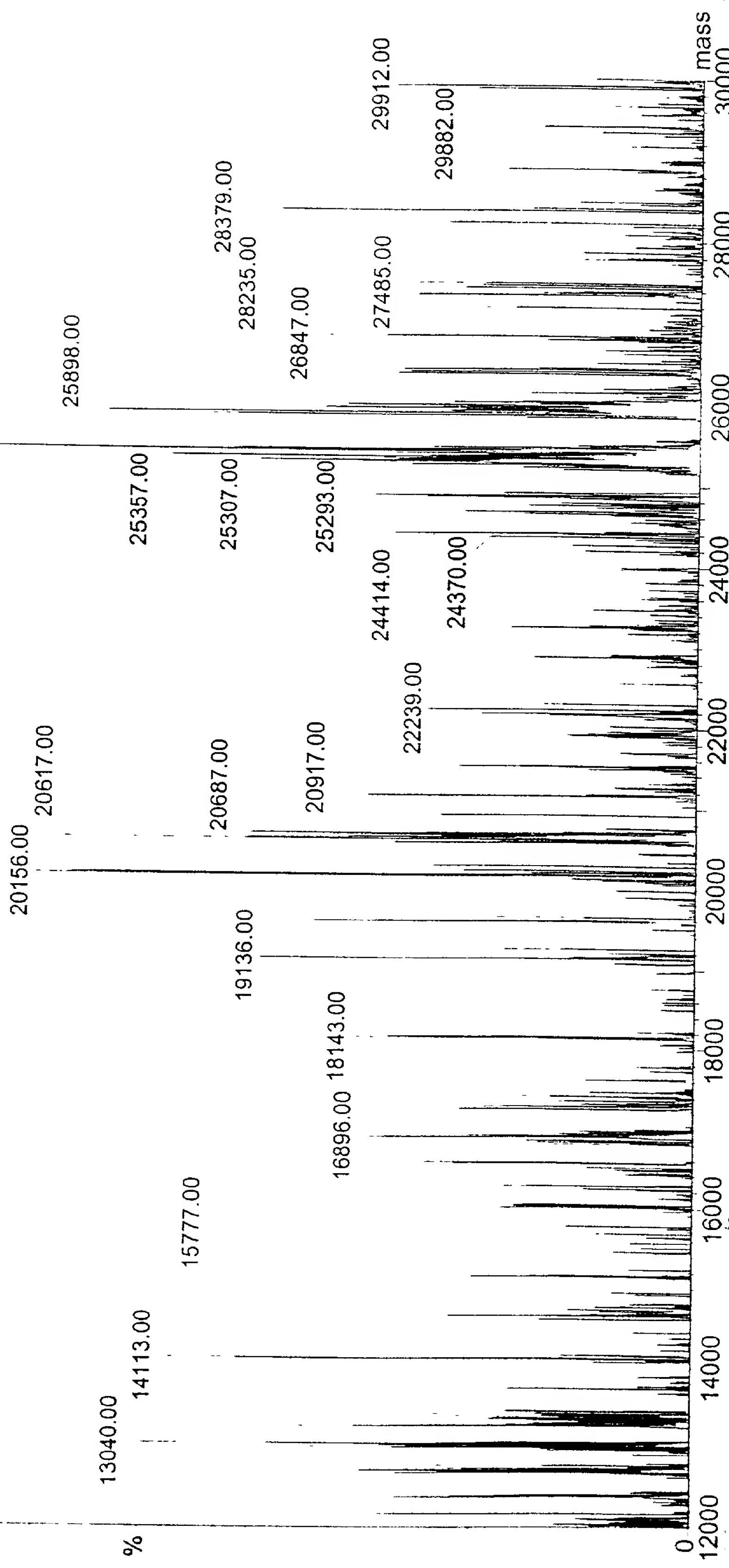


FIG. 4 (d)

GOURDIN PLANT +zt  
45.0  
QTOO-2638 20 (0.417) Mk [Ev-47894,It24] (Gs,0.750,900.1999,1.00,L33,R33); Cm (2.86)

4.0  
100  
1046.90  
963.00 981.87  
1009.01  
1017.99  
1055.87  
1056.86  
1099.01  
1107.99  
1145.99  
1073.05  
1073.93  
1148.85  
1171.93  
1273.10  
1276.21  
1302.08  
B9  
A9  
A10  
B10  
B8  
A8  
1435.77  
1464.78  
1468.11  
1471.85  
1480.62  
1524.97  
1569.14  
A7  
1640.95  
B7  
1673.85  
1693.92

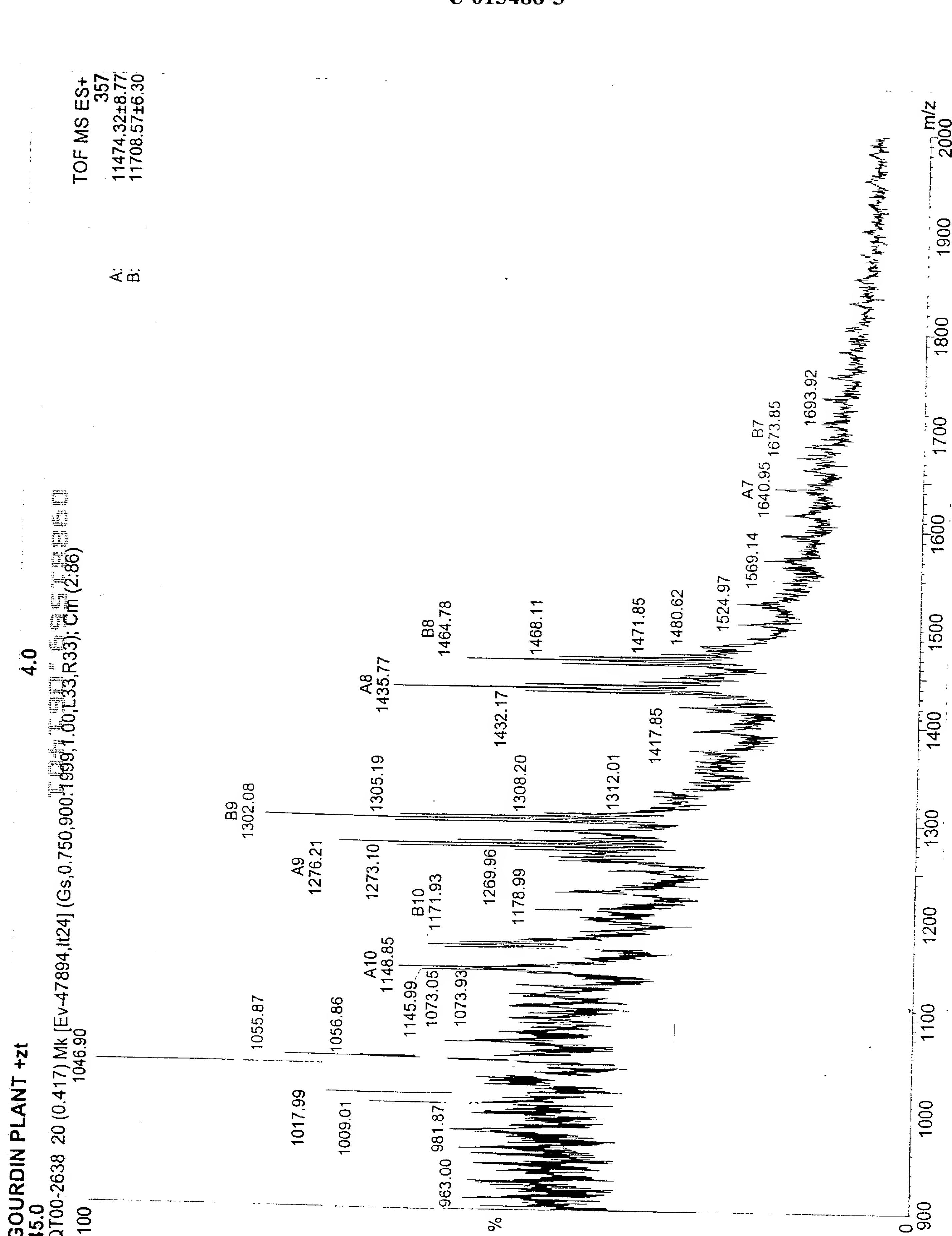
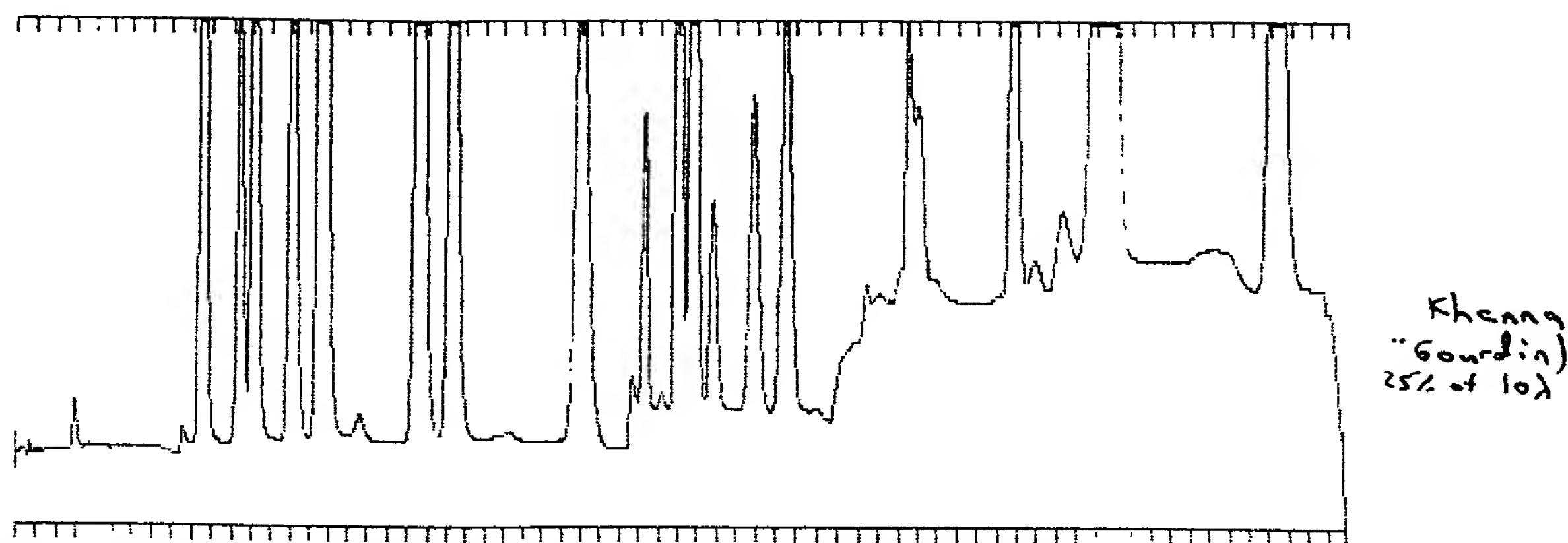


FIG. 4(e)



Interface 01 C-58 Min Scale: 15 My Ch.A, 15 My Ch.B  
 amino acid analysi Processed: 11-22-2000 14:26:30, segment 17, cycle 936  
 RAW DATA SAVED IN FILE K:AAA936.PTS Second Channel Stored in K:BAA936.PTS

#### EXTERNAL STANDARD TABLE

\*\*\*\*\* 11-22-2000 14:26:33 Version 4.1 \*\*\*\*\*  
 \* Sample Name: amino acid analysi Data File: K:AAA936 \*  
 \* Date: 11-22-2000 14:26:30 Method: F:REBECKA 11-22-2000 13:54:21 # 457 \*  
 \* Interface: 0 Cycle#: 936 Operator jmc Channel#: 0 Vial#: N.A. \*  
 \* Starting Peak Width: 21 Threshold: .5 Area Threshold: 500 \*  
 \*\*\*\*\*  
 Starting Delay: 0.00 Ending retention time: 68.00  
 Area reject: 5000 One sample per 2.002 sec.  
 Amount injected: 1.00 Dilution factor: 1.00  
 Sample Weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED			REF PEAK	% DELTA	RET TIME	CONC/AREA
				CONC	AREA	HEIGHT				
1	2.936	cysae	0.0744	0.1504%	20695	1550	13.4 1	6	-1.592	3.4373E-06
2	8.609	cysys	-0.0448	0.0866%	9566	696	13.7 1	6	0	4.2818E-06
3	9.543	asx	3.6346	7.6853%	1019304	61489	16.6 1	6	.5811	3.5658E-06
4	11.378	thr	1.1549	2.4420%	314916	15245	20.7 2	6	.1132	3.6674E-06
5	12.112	ser	2.0456	4.3254%	595007	27668	21.5 2	6	0	3.4380E-06
6	14.081	int. std.	1.0397	2.1985%	576309	23599	24.4 2	6	0	1.8041E-06
7	15.649	glx	6.6195	13.9967%	1959672	71617	27.4 2	6	.1667	3.3779E-06
8	17.651	pro->cys	(2.1133) -2.0045	6.1414%	28161	809	34.8 2	6	-.2854	1.0314E-04
9	20.554	gly	3.4509	7.2968%	1098728	36599	30.0 2	9	0	3.1408E-06
10	22.256	ala	2.8168	5.9561%	801412	25276	31.7 2	9	0	3.5148E-06
11	28.996	val	2.616	2.5700%	703543	16490	42.7 1	9 715 & 77	0	3.6541E-06
12	32.299	met	0.5625	1.1894%	157161	8772	17.9 1	16	.0101	3.5792E-06
13	33.166		0.0000	0.0000%	10132	523	19.4 1		0.0000E+00	
14	33.967	ileu	1.8404	3.8914%	535119	23330	22.3 2	16	-.0931	3.4392E-06
15	34.735	leu	3.1701	6.7031%	953284	38035	25.1 2	16	0	3.3255E-06
16	35.802	nl-std.	0.2739	0.5791%	163238	6196	26.3 2	16	0	1.6777E-06
17	37.871	tyr	1.0645	2.2508%	290327	9412	30.8 1	16	0	3.6666E-06
18	39.473	phe	1.6115	3.4075%	408260	12881	31.7 1	16	0	3.3472E-06
19	45.479	his	(1.211) 1.2633	2.6711%	203562	8185	24.9 2	16	0	6.2059E-06
20	46.013		0.0000	0.0000%	154147	5442	28.3 2		0.0000E+00	
21	50.751	lys	1.2451	2.6327%	385456	13267	29.1 2	16	0	3.2302E-06
22	51.885	+	-0.1050	0.3923%	32441	913	35.5 2	16	0	5.7275E-06
23	53.287		0.0000	0.0000%	102408	2246	45.6 2		0.0000E+00	
24	55.355	NH4	6.1666	13.0391%	3568074	61870	57.7 2	16	0	1.7279E-06
25	64.197	arg	3.5602	7.5279%	1016938	22156	45.9 1	16	0	3.5009E-06

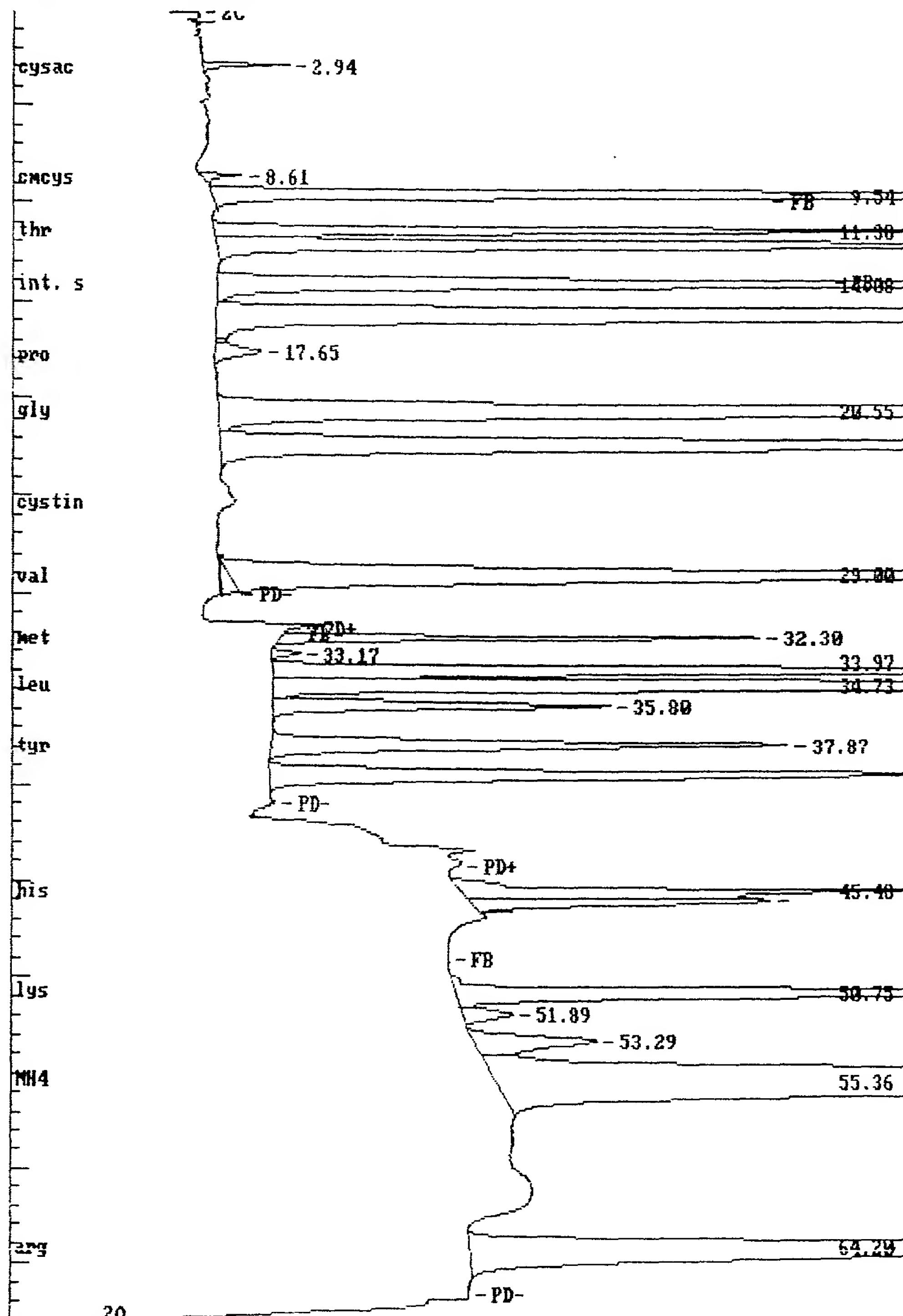
TOTAL AMOUNT :

47.2931

FIG.5(a)

# U 013488-3

Areas, times, and heights stored in: K:AAA936.ATB  
Data File = K:AAA936.PTS Printed on 11-22-2000 at 14:27:06  
Start time: 0.00 min. Stop time: 68.00 min. Offset: 0 mv.  
Full Range: 15 millivolts



## EXTERNAL STANDARD TABLE

11-22-2000 14:27:06 Version 4.1

BL-BL-BL-BL-BL

FIG.5(b)

## U 013488-3

\*\*\*\*\* Sample Name: amino acid analysis Data File: K:BAA936  
 \* Date: 11-22-2000 14:26:30 Method: F:SEBECKA 11-22-2000 13:55:21 # 25  
 \* Interface: 0 Cycle#: 936 Operator jmc Channel#: 1 Vial#: N.A.  
 \* Starting Peak Width: 21 Threshold: .5 Area Threshold: 500  
 \*\*\*\*  
 Starting Delay: 0.00 Ending retention time: 68.00  
 Area reject: 5000 One sample per 2.002 sec.  
 Amount injected: 1.00 Dilution factor: 1.00  
 Sample Weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in moles	NORMALIZED			REF PEAK	% DELTA	RET TIME	CONC/AREA
				CONC	AREA	HEIGHT				
1	8.775		0.0000	0.0000%	5143	286	18.0 1			0.0000E+00
2	9.510		0.0000	0.0000%	129394	7707	16.8 1			0.2000E+00
3	11.345		0.0000	0.0000%	24369	1171	21.3 2			0.0000E+00
4	12.079		0.0000	0.0000%	59186	2389	24.7 2			0.0000E+00
5	14.047		0.0000	0.0000%	47121	1973	23.8 1			0.3000E+00
6	15.616 glx		6.0317	74.6757%	375516	13802	27.2 1	7	.1393	1.6595E-05
7	17.651 pro+cys	(2.1133)	25.3244%	199944	6665	30.0 1	7	0	1.3570E-05	
8	20.554		0.0000	0.0000%	83582	2753	30.4 1			0.0000E+00
9	22.222		0.0000	0.0000%	67237	2027	33.2 1			0.0000E+00

TOTAL AMOUNT = 8.3451

Areas, times, and heights stored in: K:BAA936.ATB  
 Data File = K:BAA936.PTS Printed on 11-22-2000 at 14:28:59  
 Start time: 0.00 min. Stop time: 68.00 min. Offset: -95 mV.  
 Full Range: 15 millivolts

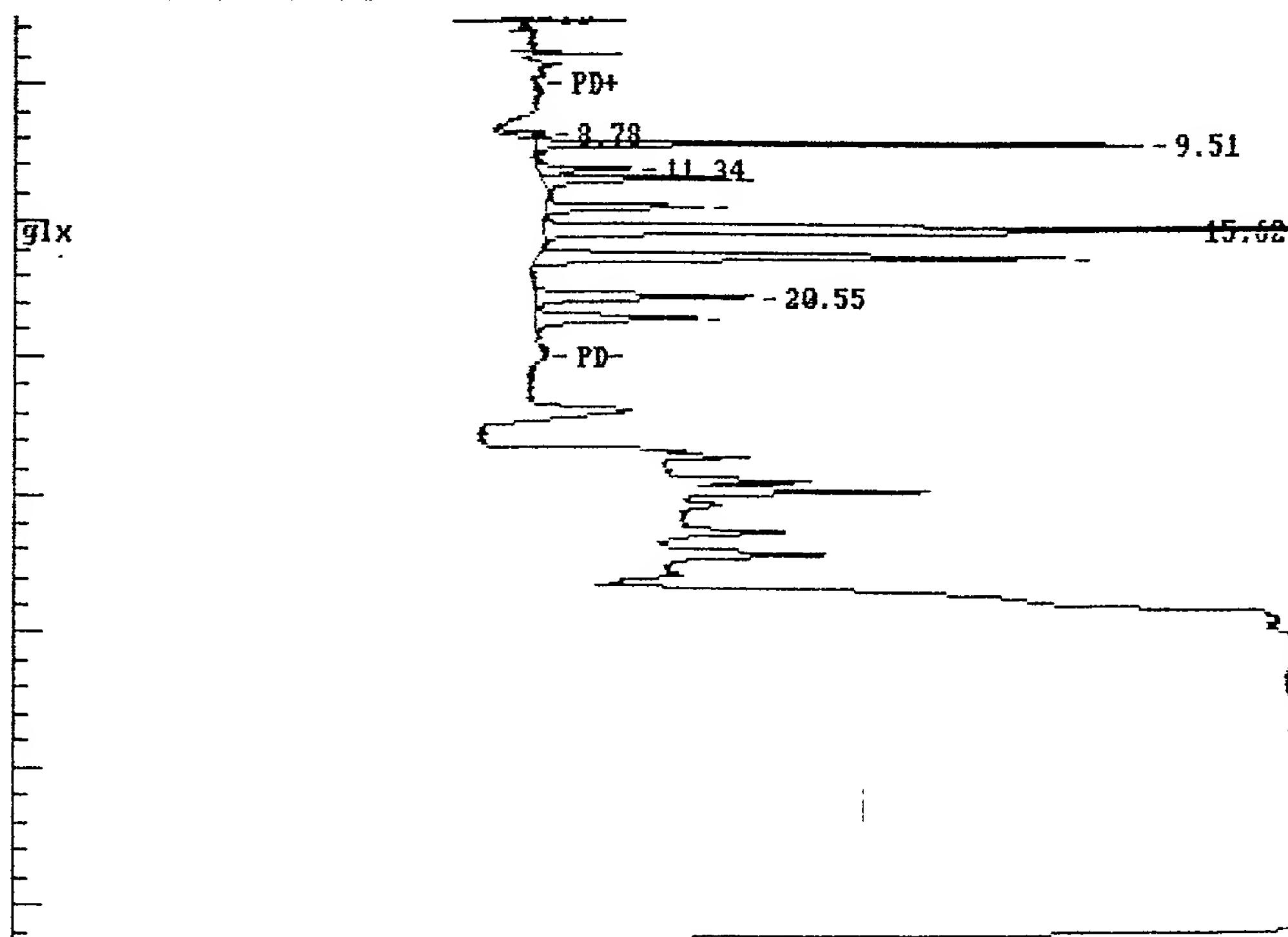


FIG.5(c)